



SEQUENCE LISTING

<110> Li, Shengwen
Kei, Aoki R.

<120> Rescue Agents for Treating a Botulinum Toxin Intoxication

<130> ALLE0004-100

<140> 10/715,810

<141> 2003-11-17

<160> 105

<170> PatentIn version 3.2

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<211> 4

<212> PRT

<213> Artificial Sequence

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<223> chemically synthesized peptide

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Xaa is any amino acid.

<400> 1

Glu Xaa Xaa His

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<210> 2

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<212> PRT

<213> Artificial sequence

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<222> (3)..(4)

<223> Xaa is any amino acid.

<400> 2

Gly Thr Xaa Xaa Asn

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5

<210> 3

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<212> PRT

<213> Artificial Sequence

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<223> chemically synthesized peptide

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Arg Gly Ser His His His His His His Gly Ser Gly Thr
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<210> 4

<211> 1302

<212> PRT

<213> Clostridium botulinum

<400> 4

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20 25 30

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140

Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145 150 155 160

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
 210 215 220
 Leu Ile Tyr Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
 225 230 235 240
 Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
 245 250 255
 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
 260 265 270
 Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
 275 280 285
 Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
 290 295 300
 Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
 305 310 315 320
 Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
 325 330 335
 Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
 340 345 350
 Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
 355 360 365
 Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
 370 375 380
 Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
 385 390 395 400
 Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
 405 410 415
 Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
 420 425 430
 Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
 435 440 445
 Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
 450 455 460

Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
 465 470 475 480
 Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
 485 490 495
 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
 500 505 510
 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 515 520 525
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
 530 535 540
 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
 545 550 555 560
 His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
 565 570 575
 Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 580 585 590
 Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
 595 600 605
 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 610 615 620
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
 625 630 635 640
 Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
 645 650 655
 Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
 660 665 670
 Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
 675 680 685
 Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
 690 695 700
 Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
 705 710 715 720

Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865 870 875 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
885 890 895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
900 905 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
915 920 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
965 970 975

Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
980 985 990

Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
995 1000 1005

Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
1010 1015 1020

Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
1025 1030 1035

Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
1040 1045 1050

Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp
1055 1060 1065

Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
1070 1075 1080

Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1085 1090 1095

Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met
1100 1105 1110

Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
1115 1120 1125

Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val
1130 1135 1140

Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
1145 1150 1155

Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
1160 1165 1170

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1175 1180 1185

Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
1190 1195 1200

Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser
1205 1210 1215

Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
1220 1225 1230

Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245

Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala
1250 1255 1260

Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1265 1270 1275

Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
1280 1285 1290

Arg Pro Leu His His His His His His
1295 1300

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<212> PRT
<213> Clostridium botulinum

<400> 5

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20 25 30

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145 150 155 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
 385 390 395 400
 Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
 405 410 415
 Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
 420 425 430
 Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
 435 440 445
 Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
 450 455 460
 Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
 465 470 475 480
 Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
 485 490 495
 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
 500 505 510
 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 515 520 525
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
 530 535 540
 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
 545 550 555 560
 His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
 565 570 575
 Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 580 585 590
 Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
 595 600 605
 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 610 615 620
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
 625 630 635 640

Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
 645 650 655
 Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
 660 665 670
 Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
 675 680 685
 Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
 690 695 700
 Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
 705 710 715 720
 Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
 725 730 735
 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
 740 745 750
 Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
 755 760 765
 Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
 770 775 780
 Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
 785 790 795 800
 Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
 805 810 815
 Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
 820 825 830
 Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
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 Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
 850 855 860
 Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
 865 870 875 880
 Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
 885 890 895

Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
 900 905 910
 Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
 915 920 925
 Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
 930 935 940
 Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
 945 950 955 960
 Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
 965 970 975
 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
 980 985 990
 Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
 995 1000 1005
 Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
 1010 1015 1020
 Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
 1025 1030 1035
 Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
 1040 1045 1050
 Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp
 1055 1060 1065
 Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 1070 1075 1080
 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 1085 1090 1095
 Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met
 1100 1105 1110
 Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
 1115 1120 1125
 Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val
 1130 1135 1140

Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
1145 1150 1155

Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
1160 1165 1170

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1175 1180 1185

Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
1190 1195 1200

Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser
1205 1210 1215

Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
1220 1225 1230

Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245

Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala
1250 1255 1260

Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1265 1270 1275

Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
1280 1285 1290

Arg Pro Leu
1295

<210> 6
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<220>
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<400> 6

Ser Phe Gly His Glu Val Leu Asn Leu Thr Arg
1 5 10

<210> 7
<211> 12
<212> PRT
<213> Artificial sequence

<220>

<223> Peptide fragment (residues 382-393)

<400> 7

Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn Leu Arg
1 5 10

<210> 8

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 394-415)

<400> 8

Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn
1 5 10 15

Asn Met Asn Phe Thr Lys
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<210> 9

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 418-427)

<400> 9

Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys
1 5 10

<210> 10

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 457-477)

<400> 10

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15

Asn Asp Leu Asn Lys
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<210> 11

<211> 59

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 478-536)

<400> 11

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
1 5 10 15

Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
20 25 30

Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
35 40 45

Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
50 55

<210> 12

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 773-779)

<400> 12

Leu Asn Glu Ser Ile Asn Lys
1 5

<210> 13

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 787-806)

<400> 13

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
1 5 10 15

Tyr Gly Val Lys
20

<210> 14

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 841-855)

<400> 14

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
1 5 10 15

<210> 15
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 872-882)
<400> 15

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
1 5 10

<210> 16
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 930-948)
<400> 16

Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
1 5 10 15

Trp Ile Arg

<210> 17
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 952-975)
<400> 17

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
1 5 10 15

Met Glu Asn Asn Ser Gly Trp Lys
20

<210> 18
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1001-1013)
<400> 18

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
1 5 10

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1024-1028)

<400> 19

Leu Asn Asn Ser Lys
1 5

<210> 20
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1086-1098)

<400> 20

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1 5 10

<210> 21
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1141-1156)

<400> 21

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
1 5 10 15

<210> 22
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1193-1204)

<400> 22

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1 5 10

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1205-1224)

<400> 23

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
1 5 10 15

Val Val Met Lys
20

<210> 24

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1261-1269)

<400> 24

Leu Val Ala Ser Asn Trp Tyr Asn Arg
1 5

<210> 25

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 20-40)

<400> 25

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15

Asn Asp Leu Asn Lys
20

<210> 26

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 41-99)

<400> 26

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
1 5 10 15

Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
20 25 30

Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
35 40 45

Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
50 55

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 336-342)

<400> 27

Leu Asn Glu Ser Ile Asn Lys
1 5

<210> 28
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 350-369)

<400> 28

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
1 5 10 15

Tyr Gly Val Lys
20

<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 404-418)

<400> 29

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
1 5 10 15

<210> 30
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 435-445)

<400> 30

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
1 5 10

<210> 31
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 493-511)

<400> 31

Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
1 5 10 15

Trp Ile Arg

<210> 32
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 515-538)

<400> 32

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
1 5 10 15

Met Glu Asn Asn Ser Gly Trp Lys
20

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 564-576)

<400> 33

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
1 5 10

<210> 34
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 587-591)

<400> 34

Leu Asn Asn Ser Lys
1 5

<210> 35
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 649-661)

<400> 35

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1 5 10

<210> 36

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 704-719)

<400> 36

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
1 5 10 15

<210> 37

<211> 12

<212> PRT

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<223> Peptide fragment (residues 756-767)

<400> 37

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1 5 10

<210> 38

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 768-787)

<400> 38

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
1 5 10 15

Val Val Met Lys
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<210> 39

<211> 859

<212> PRT

<213> Clostridium botulinum

<400> 39

Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys Ala Leu Asn Asp Leu
1 5 10 15

Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp
Page 20

20										25										30													
Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr																		
		35					40					45																					
Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln																		
	50					55					60																						
Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile																		
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Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn																		
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Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr																		
			100					105					110																				
Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg																		
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Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg																		
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Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala																		
145					150				155					160																			
Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp																		
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Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp																		
			180					185					190																				
Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn																		
		195					200					205																					
Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala																		
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Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly																		
225					230					235					240																		
Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln																		
				245					250					255																			
Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val																		
			260					265					270																				
Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	Lys	Val	Asn	Thr	Gln	Ile																		

275

280

285

Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu
 290 295 300

Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu
 305 310 315 320

Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu
 325 330 335

Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn
 340 345 350

Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val
 355 360 365

Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys
 370 375 380

Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu
 385 390 395 400

Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu
 405 410 415

Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr
 420 425 430

Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser
 435 440 445

Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly
 450 455 460

Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe
 465 470 475 480

Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val
 485 490 495

Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile
 500 505 510

Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile
 515 520 525

Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly
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530

535

540

Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val
 545 550 555 560

Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
 565 570 575

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile
 580 585 590

Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly
 595 600 605

Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg
 610 615 620

Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys
 625 630 635 640

Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn
 645 650 655

Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys
 660 665 670

Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val
 675 680 685

Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly
 690 695 700

Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly
 705 710 715 720

Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
 725 730 735

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys
 740 745 750

Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile
 755 760 765

Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val
 770 775 780

Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met
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Gly Val Thr Lys
1

<210> 43
<211> 8
<212> PRT
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<220>
<223> Peptide fragment (residues 98-105)
<400> 43

Ile Tyr Ser Thr Asp Leu Gly Arg
1 5

<210> 44
<211> 8
<212> PRT
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<400> 44

Met Leu Leu Thr Ser Ile Val Arg
1 5

<210> 45
<211> 15
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<220>
<223> Peptide fragment (residues 114-128)
<400> 45

Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
1 5 10 15

<210> 46
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 129-145)
<400> 46

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
1 5 10 15

Arg

<210> 47

<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 146-166)

<400> 47

Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile Ile
1 5 10 15
Gln Phe Glu Cys Lys
20

<210> 48
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 167-177)

<400> 48

Ser Phe Gly His Glu Val Leu Asn Leu Thr Arg
1 5 10

<210> 49
<211> 10
<212> PRT
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<220>
<223> Peptide fragment (residues 178-187)

<400> 49

Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg
1 5 10

<210> 50
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 188-212)

<400> 50

Phe Ser Pro Asp Phe Thr Phe Gly Phe Glu Glu Ser Glu Leu Val Asp
1 5 10 15
Thr Asn Pro Leu Leu Gly Ala Gly Lys
20 25

<210> 51
<211> 19
<212> PRT

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<220>

<223> Peptide fragment (residues 213-231)

<400> 51

Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu Leu Ile His Ala
1 5 10 15

Gly His Arg

<210> 52

<211> 20

<212> PRT

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<220>

<223> Peptide fragment (residues 245-264)

<400> 52

Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu Glu Val Ser Phe
1 5 10 15

Glu Glu Leu Arg
20

<210> 53

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 265-272)

<400> 53

Thr Phe Gly Gly His Asp Ala Lys
1 5

<210> 54

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 273-283)

<400> 54

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg
1 5 10

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 292-299)

<400> 55

Asp Ile Ala Ser Thr Leu Asn Lys
1 5

<210> 56

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 302-314)

<400> 56

Ser Ile Val Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys
1 5 10

<210> 57

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 321-330)

<400> 57

Tyr Leu Ser Ser Glu Asp Thr Ser Gly Lys
1 5 10

<210> 58

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 331-335)

<400> 58

Phe Ser Val Asp Lys
1 5

<210> 59

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 344-356)

<400> 59

Met Leu Thr Glu Ile Tyr Thr Glu Asp Asn Phe Val Lys
1 5 10

<210> 60
<211> 7
<212> PRT
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<400> 60

Thr Tyr Leu Asn Phe Asp Lys
1 5

<210> 61
<211> 12
<212> PRT
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<223> Peptide fragment (residues 382-393)

<400> 61

Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn Leu Arg
1 5 10

<210> 62
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<212> PRT
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<220>
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<400> 62

Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn
1 5 10 15

Asn Met Asn Phe Thr Lys
20

<210> 63
<211> 10
<212> PRT
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<220>
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<400> 63

Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys
1 5 10

<210> 64
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<212> PRT
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<400> 64

Gly Ile Ile Thr Ser Lys
1 5

<210> 65
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<220>
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<400> 65

Asn Asp Gln Gly Ile Thr Asn Lys
1 5

<210> 66
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<400> 66

Ser Leu Asp Lys
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<210> 67
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<223> Peptide fragment (residues 457-477)

<400> 67

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15

Asn Asp Leu Asn Lys
20

<210> 68
<211> 59
<212> PRT
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<223> Peptide fragment (residues 478-536)

<400> 68

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
 1 5 10 15
 Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
 20 25 30
 Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
 35 40 45
 Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
 50 55

<210> 69
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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 <400> 69

Tyr Thr Met Phe His Tyr Leu Arg
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<210> 70
 <211> 20
 <212> PRT
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<220>
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 <400> 70

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
 1 5 10 15
 Val Val Met Lys
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<210> 71
 <211> 16
 <212> PRT
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 <400> 71

Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg
 1 5 10 15

<210> 72
 <211> 11
 <212> PRT
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<220>

<223> Peptide fragment (residues 582-592)

<400> 72

Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
1 5 10

<210> 73

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 597-626)

<400> 73

Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr
1 5 10 15

Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys
20 25 30

<210> 74

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 627-649)

<400> 74

Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn
1 5 10 15

Ile Gly Asn Met Leu Tyr Lys
20

<210> 75

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 650-688)

<400> 75

Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu Leu
1 5 10 15

Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala Leu
20 25 30

Val Ser Tyr Ile Ala Asn Lys
35

<210> 76

<211> 13

<212> PRT
 <213> Artificial Sequence

 <220>
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 <400> 76
 Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys
 1 5 10

<210> 77
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Peptide fragment (residues 712-720)

 <400> 77
 Tyr Ile Val Thr Asn Trp Leu Ala Lys
 1 5

<210> 78
 <211> 9
 <212> PRT
 <213> Artificial Sequence

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 <223> Peptide fragment (residues 721-729)

 <400> 78
 Val Asn Thr Gln Ile Asp Leu Ile Arg
 1 5

<210> 79
 <211> 11
 <212> PRT
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 <220>
 <223> Peptide fragment (residues 734-744)

 <400> 79
 Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys
 1 5 10

<210> 80
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Peptide fragment (residues 745-759)

 <400> 80

Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys
1 5 10 15

<210> 81
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 760-772)

<400> 81

Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys
1 5 10

<210> 82
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 773-779)

<400> 82

Leu Asn Glu Ser Ile Asn Lys
1 5

<210> 83
<211> 20
<212> PRT
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<220>
<223> Peptide fragment (residues 787-806)

<400> 83

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
1 5 10 15

Tyr Gly Val Lys

<210> 84
<211> 9
<212> PRT
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<223> Peptide fragment (residues 808-816)

<400> 84

Leu Glu Asp Phe Asp Ala Ser Leu Lys
1 5

<210> 85
<211> 9

<212> PRT
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<223> Peptide fragment (residues 828-836)

<400> 85

Gly Thr Leu Ile Gly Gln Val Asp Arg
1 5

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 841-855)

<400> 86

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
1 5 10 15

<210> 87
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 862-871)

<400> 87

Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys
1 5 10

<210> 88
<211> 11
<212> PRT
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<220>
<223> Peptide fragment (residues 872-882)

<400> 88

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
1 5 10

<210> 89
<211> 11
<212> PRT
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<220>
<223> Peptide fragment (residues 883-893)

<400> 89

Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
1 5 10

<210> 90
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<212> PRT
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<400> 90

Tyr Ala Ser Lys
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<210> 91
<211> 6
<212> PRT
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<400> 91

Ile Asn Ile Gly Ser Lys
1 5

<210> 92
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<400> 92

Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
1 5 10

<210> 93
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Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
1 5 10 15

Trp Ile Arg

<210> 94
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<400> 94

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
1 5 10 15
Met Glu Asn Asn Ser Gly Trp Lys
20

<210> 95
<211> 19
<212> PRT
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<220>
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<400> 95

Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln
1 5 10 15
Glu Ile Lys

<210> 96
<211> 13
<212> PRT
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<223> Peptide fragment (residues 1001-1013)

<400> 96

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
1 5 10

<210> 97
<211> 10
<212> PRT
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<220>
<223> Peptide fragment (residues 1014-1023)

<400> 97

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
1 5 10

<210> 98
<211> 5
<212> PRT
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<223> Peptide fragment (residues 1024-1028)

<400> 98

Leu Asn Asn Ser Lys
1 5

<210> 99
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<212> PRT
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<220>
<223> Peptide fragment (residues 1035-1056)

<400> 99

Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
1 5 10 15

Asn Asn Ile Met Phe Lys
20

<210> 100
<211> 4
<212> PRT
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<220>
<223> Peptide fragment (residues 1062-1065)

<400> 100

Asp Thr His Arg
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<210> 101
<211> 13
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<223> Peptide fragment (residues 1086-1098)

<400> 101

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1 5 10

<210> 102
<211> 16
<212> PRT
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<220>
<223> Peptide fragment (residues 1141-1156)

<400> 102

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
1 5 10 15

<210> 103
<211> 12
<212> PRT
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<223> Peptide fragment (residues 1193-1204)
<400> 103

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1 5 10

<210> 104
<211> 6
<212> PRT
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<400> 104

Tyr Ala Ser Gly Asn Lys
1 5

<210> 105
<211> 20
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<223> Peptide fragment (residues 1277-1296)
<400> 105

Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly
1 5 10 15

Glu Arg Pro Leu
20